N N N N	m m r	<b>, , , , , , , , , , , , , , , , , , , </b>
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM protein - protein search, using sw model	February 1, 2005, 14:15:38; Search time 166 Seconds (without alignments) 522.967 Million cell updates/sec
	OM prote	Run on:

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Title: Perfect acore:	US-10-629-329A-2 1322	
Sequence:	1 MSGCDAGEGDCCSRRCGAQDSMKKVGLDPSQLPVGENGIV 242	242
Scoring table: BLOSUM62	BLOSUM62	

2002273 segs, 358729299 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

2002273

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqp1980s:\*
geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2001s:\*
geneseqp2003s:\*
geneseqp2003bs:\*
geneseqp2003bs:\* A\_Geneseq\_23Sep04:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	Adi62654 Human ran		Amin	•			Aay85635 Antigen r		Aau78361 Cell diff	Adi62656 Mouse ran		Abo55349 Human gen		Aag74374 Human col			Abu27936 Protein e	Abo81414 Pseudomon	Abul5639 Protein e	Abo66904 Klebsiell	Abu02540 S. pneumo	Abu31958 Protein e	Abu46266 Protein e	Aay70730 Klebsiell	
SUMMAKIES	OI	ADJ62654	AAU78360	AAG67127	AAW94762	AAY85636	AAU77178	AAY85635	AAU77177	AAU78361	ADJ62656	ABB65485	AB055349	AA010783	AAG74374	ABU17451	ABU41912	ABU27936	AB081414	ABU15639	ABO66904	ABU02540	ABU31958	ABU46266	AAY70730	ABU21860
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Adk48234 Streptoco Adm26979 Hyperther Abp27712 Streptoco		Addagos Flocain e Adc3450 E. faeciu Abp65425 Bifidobac Abu28874 Protein e		Aaw22376 S. pneumo Adk47774 Streptoco Abu29217 Protein e Adh88180 Enteroco	Abu25094 Protein e Adn47255 Thermococ
ADK48234 ADM26979 ABP27712	ABU46430 ABU47361 ABU18884	ABC94690 ABC65425 ABU28874	ABU49976 ABU29712 ADC95935 ABU49674	AAW22376 ADK47774 ABU29217 ADH88180	ABU25094 ADN47255
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## ALIGNMENTS

rank-associated inhibitor; RAIN protein; osteopathic; bone loss; human; chromosome 11. Human rank-associated inhibitor (RAIN) protein SEQ'ID NO:2 ADJ62654 standard; protein; 242 AA. 29-JUL-2003; 2003WO-US023801. 29-JUL-2002; 2002US-0399205P. 06-MAY-2004 (first entry) WO2004011620-A2. Homo sapiens. 05-FEB-2004. ADJ62654; ADJ6265 

(TEXA ) UNIV TEXAS SYSTEM. Darnay BG;

New isolated Rank-Associated Inhibitor (RAIN) polypeptides, useful for treating a subject with bone loss by inhibiting osteoclast precursor cell fusion. WPI; 2004-143848/14. N-PSDB; ADJ62653.

Claim 1; SEQ ID NO 2; 97pp; English.

The present invention describes an isolated polypeptide containing at least 10 contiguous amino acids of a rank-associated inhibitor (RAIN) protein. Also described. (1) an isolated polynucleotide comprising a nucleic acid encoding a RAIN polypeptide; (2) a method of treating a subject with bone loss comprising inhibiting osteoclast precursor cell tusion by administering a RAIN polypeptide to modulate RANK signaling, or an expression vector comprising the polynucleotide under the transcriptional control of a promoter; (3) a method for inhibiting osteoclast precursor cell fusion by contacting an osteoclast precursor cell with an expression vector that expresses a RAIN polypeptide; and (4) a method for identifying a modulator of an osteoclast precursor fusion by

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providing a cell deficient in a RAIN polypeptide; contacting the cell with a candidate substance; and comparing osteoclast cell fusion observed when the candidate substance is not added, where the alteration in osteoclast cell fusion indicates that the candidate substance is a modulator of an osteoclast cell fusion. RAIN sequences have osteopathic activities, and can be used for inhibiting osteoclast precursor cell fusion. The RAIN polypeptide, expression vector and methods are useful for treating a subject with bone loss. The present sequence represents invention. The human RAIN gene is located on chromosome il, more specifically to 11p12-13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cartilage cell differentiation stimulator; osteopathic; Membrane-bound transferrin-like protein; MTf-BP; concanavalin A; ConA; membrane bound type transferrin-like protein; MTf; cartilage disorder; bone metabolism disease; cell differentiation; cell growth; extracellular matrix related disease; human.
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                                                                                                                                                                                                                                                                                       1 MSGCDAGEGDCCSRRCGAQDKEHPRYLIPELCKQFYHLGWVTGTGGGISLKHGDEIYIAP
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100.0%; Pred. No. 3.1e-137
ive 0; Mismatches 0;
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                                                                                                                                                                                                  Sequence 242 AA;
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                                        The invention describes a cartilage cell differentiation stimulator (Containing a membrane-bound transferrin-like protein (WTf-BP) and a membrane bound type transferrin-like protein (WTf) and an animal-derived concanavalin-like drug. The cartilage differentiation stimulator can be used in diagnosis, prevention and treatment of cartilage and bone metabolism diseases. They can also be used for diagnosing biophylaxis, cell differentiation, cell growth and construction of extracellular matrix related diseases. MTf-BP strongly stimulates differentiation of cartilage cells and exhibits similar action mechanism with that of plant derived Conh. This is the amino acid sequence of a cartilage cell differentiation stimulator associated polypeptide described in the
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Alzheimer's disease; Pick's disease; Huntington's disease; dementia;
multiple sclerosis; Parkinson's disease; amyotropic lateral sclerosis;
meningitis; schizophranic disorder; neuroskeletal disorder; allergy;
addison's disease; autoimmune disease; anemia; asthma; Crohn's disease;
adult respiratory distress syndrome; atopic dermatitis; psoriasis;
diabetes mellitus; osteoporosis; pancreatitis; rheumatoid arthritis;
infection; genetic disorder; muscular dystrophy; Gaucher's disease;
Huntington's chorea; sickle cell anemia; thalassemia; atherosclerosis;
von Willebrand's disease; Wilms' tumour; cell proliferative disorder;
leukemia; hepatitis; cirrhosis; arteriosclerosis; gene therapy.
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                                                                                                                                                                                                                                                                                                                               Gaps
                                       describes a cartilage cell differentiation stimulator
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                                                                                                                                                                                                                                                                                              Length 242;
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Pred. No. 2.4e-136;
0; Mismatches 1;
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            Claim 2; Page 8-9; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                 99.4%;
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Best Local Similarity 99.6
Matches 241; Conservative
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                                                                                                                                                                                                                                                                   Sequence 242 AA;
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The present sequence represents a human enzyme. The enzyme polymucleotide and polypeptide are useful for diagnosis, treatment and prevention of cancers, neurological disorders (e.g. epilepsy, stroke, Alzhaimer's disease, Plck's disease, Huntington's disease, dementia, multiple sclerosis, Parkinson's disease, amyotropic lateral sclerosis, bacterial and viral meningitis, schizophrenic disorders and neuroskeletal and sorters, autoimmune/inflammatory disorders (e.g. allergies, addison's disease, autoimmune disease, atopic dermatitis, diabetes mellitus, onemnia, asthma, Crohn's disease, atopic dermatitis, diabetes mellitus, coreoporosis, parasitic, protozoal and helminthic infections), genetic disorder (e.g. Duchenne and Becker muscular dystrophy, Gaucher's disease, Huntington's chorea, sickle cell anemnia, thalassemia, Von Willebrand's disease and Wilms' tumour), and cell proliferative disorder (e.g. atherosclerosis, leukemia, hepatitis, cirrhosis, and discase and Wilms' tumour), and cell proliferative disorder (e.g. atherosclerosis, leukemia, hepatitis, cirrhosis, and discase and wilms' tumour) and sell in somatic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human enzyme molecule useful for treating and preventing, e.g., cancer, genetic disorders, neurological disorders, autoimmune and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burford N;
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                                                                                                                                                                                              /note= "potential phosphorylation site"
209
"potential phosphorylation site"
                                   note= "potential phosphorylation site"
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216
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Pred. No. 1.4e-135;
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98.9%; Score 1307; D
Best Local Similarity 99.2%; Pred. No. 1.4e
Matches 240; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2000; 2000US-0186307P.
28-MAR-2000; 2000US-0192532P.
30-MAR-2000; 2000US-0193578P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lu DAM, Bandman O,
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167
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   note=
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N-PSDB; AAH75155.
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                   Modified-site
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Baughn MR;
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This represents the amino acid sequence of human HFIZG53. Host cells containing an expression system comprising the HFIZG53 nucleic acid are used for the recombinant production of the protein. HFIZG53 polypeptides are useful for diagnosing diseases related to over or underexpression of HFIZG53 protein. The HFIZG53 polypeptides can be used to cream for agonists and antergonists which can be used in treatment to activate or inhibit HFIZG53 activity. Gene therapy may also be used to affect endogenous polypeptide production, using HFIZG53 polynucleotides are and retroviral vectors. HFIZG53 antibodies are useful for inducing an immune response to immunise and prevent diseases, and for isolating HFIZG53 clones or purifying the polypeptide by affinity chromatography. HFIZG53 polypeptides can be administered directly or as a vaccine to inoculate against disease. Diseases prevented, diagnosed or treated include inflammatory diseases nuch as Adult Respiratory Disease Syndrome, thoumatoid arthritis, osteoarthritis, inflammatory Bowel Disease Syndrome, procused and viral, particularly HVV-1 and -2; HIV-associated cachexia and other immunodeficiency disorders; septic shock; injury; pain; cancers
SGVQKERIQPEDMFVCDINEKDISGPSPSKKLKKSQCTPLFMNAYTWRGAGAVIHTHSKA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HFIZG53; human; inflammatory disease; infection; HIV-1; HIV-2; cancer; HIV-associated cachexia; immunodeficiency disexder; septic shock; pain; HIV-associated cachexia; immunodeficiency disexder; septic shock; pain; Parkinson's disease; cardiovascular disease; psychotic; neurological; Huntington's disease; Gilles de la Tourette's syndrome; gene mapping.
                                                      MNEYPDSCAVLVRRHGVYVWGETWEKAKTMCECYDYLFDIAVSMKKVGLDPSQLPVGENG
                                                                                                           MNEYPDSCAVLVRRHGVYVWGETWEKAKTMCECYDYLFDIAVSMKKVGLDPSQLPVGENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New HFIZG53 polypeptide and polynucleotide - useful as diagnostic reagents and for prevention and treatment of inflammatory diseases, cancer and Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of human HFIZG53.
                                                                                                                                                                                                                                                                                                                   AAW94762 standard; protein; 242 AA
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N-PSDB; AAX05748.
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including testicular cancer; anorexia; bulimia; Parkinson's disease; cardiovascular disease including restenosis, atherosclerosis, acute heart failure, myocardial infarction, hypotension, hypotension, urinary retention; angina pectoris; ulcers; benign prostatic hypertrophy; and psychotic and neurological disorders (anxiety, schizophrenia, delirium, manic depression, dementia, severe mental retardation) and dyskinesias, such as Hutington's diseases or Gilles de la Tourette's syndrome. The HRIZGS3 polypeptide is also useful for mapping the gene to a chromosome, allowing gene inheritance to be studied through linkage analysis
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                                                                                                                                                                         Length 242;
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                                                                                                                                                                         / Match 98.0%; Score 1296; DB 2; Local Similarity 98.8%; Pred. No. 2.3e-134; hes 239; Conservative 0; Mismatches 3;
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Gene encoding an antigen recognizing an antibody which induces granulocyte colony stimulating factor (G-CSF) expression for gene therapy and treatment of G-CSF associated disorders e.g. the side effects of

Aoki Y, Nishi 2001-024452/03.

Sha S,

N-PSDB; AAC61150

Claim 3; Page 52-53; 58pp; Japanese.

cancer therapy

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The present invention relates to a gene encoding an antigenic protein recognised by an antibody or its fragments which can induce the production of granulacyte colony stimulating factor (G-CSF). Also included in the invention are partial sequences of the gene, antibodies recognising all or part of the antigenic protein, expression vectors containing the gene and host cells transformed by the vector. The gene used for gene therapy, and compounds identified by screening using the gene sequence are used for treatment and prevention of disorders associated with G-CSF expression such as the side effects of cancer therapy (including bone marrow suppression). The present sequence represents the human antigen of the invention
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0
                                                                                                                                                                                                                      Length 242;
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                                                                                                                                                                                                                    98.0%; Score 1296; DB 4;
98.8%; Pred. No. 2.3e-134;
iive 0; Mismatches 3;
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                                                                                                                                                                                                                                     Best Local Similarity 98.8
Matches 239; Conservative
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2; Page 49-50; 58pp; Japanese.
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Best Local Similarity 93.8'
Matches 227; Conservative
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N-PSDB; ABK47966.
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                                                            The invention relates to a mouse or human gene (MMR19) encoding a protein which binds to antibodies or their fragments which induce granulocytecolony stimulating factor (G-CSF) secretion. The genes and proteins of the invention are used in diagnosis, treatment and prevention of diseases associated with G-CSF, including infections and neutrophil deficiency disease. This sequence represents a human G-CSF-inducible antibody binding protein, MMR19
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                                                                                                                                                                                                                                                                                         98.0%; Score 1296; DB 5; Length 242; 98.8%; Pred. No. 2.3e-134;
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                                                                                                                                                                                                                                                                                                                                    Indels
potential drugs treating G-CSF associated diseases.
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                                         Claim 3; Page 96-97; 103pp; Japanese.
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The present invention relates to a gene encoding an antigenic protein recognised by an antibody or its fragments which can induce the production of granulocyte colony stimulating factor (G-CSF). Also included in the invention are partial sequences of the gene, antibodies recognising all or part of the antigenic protein, expression vectors containing the gene and host cells transformed by the vector. The gene used for gene therapy, and compounds identified by screening using the gene are used for treatment and prevention of disorders associated with G-CSF expression such as the side effects of cancer therapy (including bone marrow suppression). The present sequence represents the murine antigen of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 MNEYPDSCAVLVRRHGVYVWGETWEKAKTMCECYDYLFDIAVSMKKMGLDFJQLPVGENG 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 MNEYPDSCAVLVRRHGVYVWGETWEKAKTMCECYDYLFDIAVSMKKVGLDPSQLPVGENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSGCDAGEGDCCSRRCGAQDKEHPRYLIPELCKQFYHLGWVTGTGGGISLKHGDEIYIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGVQKERIQPEDMFVCDINEKDISGPSPSKKLKKSQCTPLFMNAYTMRGAGAVIHTHSKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%; Score 1239.5; DB 4
93.8%; Pred. No. 4.1e-128;
iive 9; Mismatches 5;
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invention
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                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                       Query Match
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                                                                     which binds to antibodies or their fragments which induce granulocyte-colony stimulating factor (G-GSF) secretion. The genes and proteins of the invention are used in diagnosis, treatment and prevention of diseases associated with G-GSF, including infections and neutrophil deficiency disease. This sequence represents a mouse G-GSF-inducible antibody
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                                                                                                                                                                                                                                                                                                                                                  239
                                                            encoding a protein
                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cartilage cell differentiation stimulator useful in the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cartilage cell differentiation stimulator; osteopathic; Membrane-bound transferrin-like protein; MTf-BP; concanavalin A; ConA; membrane bound type transferrin-like protein; MTf; cartilage disorder; bone metabolism disease; call differentiation; cell growth; extracellular matrix related disease; mouse.
                                                                                                                                                                                                                                                            SGVQKERIQPEDMFVCDINEQDISGPPASKKLKKSQCTPLFMNAYTWRGAGAVIHTHSKA
                                                                                                                                                                                                                  SGVOKERIOPEDMFVCDINEKDISGPSPSKKLKKSQCTPLFMNAYTMRGAGAVIHTHSKA
                                                                                                                                                                                                                                                                                      AVMATLLFPGREFKITHQEMIKGIKKCTSGGYYRYDDMLVVPIIENTPEEKGLKDRMAHA
                                                                                                                                                                                                                                                                                                   MSGCDAGEGDCCSRRCGAODKEHPRYLIPELCKOFYHLGWVTGTGGGISLKHGDEIYIAP
                                                                                                                                                                                                                                                                                                                              MNEYPDSCAVLVRRHGVYVWGETWEKAKTMCECYDYLFDIAVSMKKVGLDPSQLPVGENG
                                                                                                                                                                                   Gaps
Gene encoding protein binding to antibody having granulocyte-colony stimulating factor (G-CSF) inducing activity, useful for screening potential drugs treating G-CSF associated diseases.
                                                                                                                                                                                   1;
                                                                                                                                                               Length 241;
                                                                                                                                                               Score 1239.5; DB 5; Length
Pred. No. 4.1e-128;
9; Mismatches 5; Indels
                                                             (MMR19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell differentiation stimulator associated protein #2.
                                                             to a mouse or human gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                          Claim 1; Page 93-94; 103pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU78361 standard; protein; 241 AA
                                                                                                                                                                                   6
                                                                                                                                                                93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000; 2000JP-00206566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                               Query Match 93.8
Best Local Similarity 93.8
Matches 227; Conservative
                                                                                                               disease. This sequence
binding protein, MMR19
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                                                                                                                                                                                                                                                                                                                                                                                           241
                                                                                                                                             Sequence 241 AA
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(containing a membrane-bound transferrin-like protein (MTF-BP) and a membrane bound type transferrin-like protein (MTf) and an animal derived concanavalin-like drug. The cartilage differentiation stimulator can be used in diagnosis, prevention and tradtment of cartilage and bone metabolism diseases. They can also be used for diagnosing biophylaxis, cell differentiation, cell growth and construction of extracellular matrix related diseases. WTF-BP strongly stimulates differentiation of cartilage cells and exhibits similar action mechanism with that of plant derived ConA. This is the amino acid sequence of a cartilage cell differentiation stimulator associated polypeptide described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 SGVQKERIQPEDMFVCDINEQDISGPPASKKLKKSQCTPLFMNAYTWRGAGAVIHTHSKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSGCQA-QGDCCSRPCGAQDKEHPRFLIPELCKQFYHLGWVTGTGGGISLKHGNBIYIAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AVMATLLFPGREFKITHQEMIKGIKKCTSGGYYRYDDMLVVPIIENTPEEKGLKDRMAHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNEYPDSCAVLVRRHGVYVWGETWEKAKTMCECYDYLFDIAVSMKKVGLDPSQLPVGENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSGCDAGEGDCCSRRCGAQDKEHPRYLIPELCKQFYHLGWVTGTGGGISLKHGDEIYIAP
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of
                                                                                                                                                             describes a cartilage cell differentiation stimulator
            biophylaxis, cell differentiation, cell growth and construction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1239.5; DB 5; Length 241; Pred. No. 4.1e-128; 9; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse rank-associated inhibitor (RAIN) protein SEQ ID NO:4
                                            extracellular matrix related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ62656 standard; protein; 241 AA.
                                                                                                         Claim 2; Page 9-10; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-2002; 2002US-0399205P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 227; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004011620-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IV 241
                                                                                                                                                                      invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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82 DISGPSPSKKLKKSQCTPLFMNAYTMRGAGAVIHTHSKAAVMATLLFPGREFKITHQEMI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 EHPRHLIPSLCRQPYHLGWVTGTGGGMSIKYNDEIYJAPSGVQKERMQPEDLFVQDITGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 EHPRYLIPELCKOFYHLGWVTGTGGGISLKHGDEIYIAPSGVQKERIQPEDMFVCDINEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGIKKCTSGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 23247; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.8%; Score 790; DB 4; Length 227; 70.3%; Pred. No. 2e-78; ive 19; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome derived single exon protein #1583.
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                                                                                                                                                                                                                                                                      Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABO55349 standard; protein; 64 AA.
                                                                                                                                                                                                                                                                   PWD,
                                                                                                23-MAR-2001; 2001WO-US009231
                                                                                                                                              23-MAR-2000; 2000US-0191637P
                                                                                                                                                                     11-JUL-2000; 2000US-00614150
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Best Local Similarity 70.3
Matches 149; Conservative
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                                                                                                                                                                                                                                                                   Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75.
                                                                                                                                                                                                                     (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABL09588
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WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                              interactions.
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                                                27-SEP-2001
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                                                                                                                                                                                                      The present invention describes an isolated polypeptide containing at least 10 contiguous amino acids of a rank-associated inhibitor (RAIN) protein. Also described: (1) an isolated polymuclecide comprising a containing at RAIN polypeptide; (2) a method of treating a subject with bone loss comprising inhibiting osteoclast precursor cell fusion by administering a RAIN polypeptide; (2) a method of treating a comprising the polymuclecide under the transcriptional control of a promoter; (3) a method for inhibiting can expression vector comprising the polymucleotide under the precursor cell fusion by contacting an osteoclast precursor cell with an expression vector that expresses a RAIN polypeptide; and (4) a method for identifying a modulator of an osteoclast precursor fusion by providing a cell deficient in a RAIN polypeptide; contacting the cell containing a cell deficient in a RAIN polypeptide; contacting the cell contacting the cell contacting an expectation in the candidate substance; and comparing osteoclast cell fusion observed when the candidate substance; and comparing osteoclast cell fusion. RAIN sequences have osteopathic activities, and can be used for inhibiting osteoclast precursor cell continities, and can be used for inhibiting osteoclast precursor cell contracting a subject with a seemplification of the present continents. The RAIN which is used in the exemplification of the present invention. The mouse RAIN when the sequence represents invention. The mouse RAIN gene is located on chromosome 2.
                                                     New isolated Rank-Associated Inhibitor (RAIN) polypeptides, useful for treating a subject with bone loss by inhibiting osteoclast precursor cell fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGVQKERIQPEDMFVCDINEKDISGPSPSKKLKKSQCTPLFMNAYTMRGAGAVIHTHSKA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSGCDAGEGDCCSRRCGAQDKEHPRYLIPELCKOFYHLGWVTGTGGGISLKHGDEIYIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSGCQA-QGDCCSRPCGAQDKEHPRFLIPELCKQFYHLGWYTGTGGGISLKHGNEIYIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 MNEXPDSCAVLVRRHGVYVWGETWEKAKTMCECYDYLPDIAVSWKKWGLDPTQLPVGENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.8%; Score 1239.5; DB 8; Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 23247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.1e-128;
9; Mismatches 5;
                                                                                                                                                             Claim 1; SEQ ID NO 4; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB65485 standard; protein; 227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 93.8
Matches 227; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; de
pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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RESULT 11 ABB65485

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16-OCT-2003.

Penn SG,

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to tyokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hemmatopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 24675; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 273.5; DB 4
Pred. No. 1.2e-21;
3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSGCDAGEGDCCSRRCGAQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.7%; Scu.
49.1%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG74374 standard; protein; 59 AA.
                                                                          Human polypeptide SEQ ID NO 24675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAI90714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 129 AA;
                                                                                                                                                                                                                                                                                                                            WO200164835-A2.
                                                                                                                                                                                                                                                                            Homo sapiens
                         06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                   07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG74374;
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셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide acid expression, comprising any of the 27,400 fully defined nucleotide and endeds of any of the 6888 amino acid sequences on concoling at least 8 amino acids of any of the 6888 amino acid sequences concoling at least 8 amino acids of any of the 6888 amino acid sequences ("Illy defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expression (comprising a plurality of single exon mucleic acid probes cited above, where each of the plurality of probes is separately can addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acids substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to methods of selling and/or licensing single exon probes or microarrays to entered antibody that binds specifically to a peptide cited above, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying than many gene expression data by subscription, and a computer-readable catched above. The probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying generate apower. The probes are used in in identifying and characterising grown alterations in the genomic locus that includes their exon, or in constructing genome-easing the Offerenceded peptide. The sequence data for this patent did not for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 YRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWGETWEKAKTM 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 YRYDDMLVVPIIENTPEEKDLKDRMAHAMNEYPDSCAVLVRRHGVYVWGETWEKAKTM 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 312; DB 8; Length 64;
Pred. No. 2.4e-26;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 45; SEQ ID NO 28983; 80pp; English.
                                                                                                                                                                                                                                                                               Hanzel DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.6%;
                                                           03-APR-2002; 2002US-00029386.
                                                                                                                  03-APR-2002; 2002US-00029386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.6 Best Local Similarity 98.3 Matches 57; Conservative
                                                                                                                                                                  (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                               Rank DR,
                                                                                                                                                                                                                                                                                                                                     WPI; 2004-119264/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surveying tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 64 AA;
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20 MSGCNARKGDCCSRRCGSHLXNXIPTDWPLNXFFLTSAKVKECFPKKESIYSQTVYXSPG 79
                                                                                                                                                                                                                                                               Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                       63
                                         20 -----DKEHPRYLIPELCKQFYHLGWVTGTGGGISLKHGDBIYIAPSGV
                                                                                                                                                                                                                                  Human colon cancer antigen protein SEQ ID NO:5138.
                                                                                                                                                                                                         03-SEP-2001 (first entry)
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AAO10783 standard; protein; 129 AA.

RESULT 13 AA010783

ò 셤 AA010783;

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Gaps

47;

Indels

4; Length 129;

-- 19

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid concluded are:

(2) a vector comprising a promoter operably linked to the nucleic acid concludes by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product is sentially a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for to which each of the strains is present in a culture or collection of strains of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. dantifying proteins or screening condidate molecules for rational cultured patent did not form pat of the printed specification, but was obtained patent and incellular proliferation of the printed specification, but was obtained to be a compound and a procession of the printed specification, but was obtained and the contract of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 LGVPVLETELRPSAETILHTHIYNNTNAGCVLHVHTTDNNVITNLY-SDAVTLQNQEIIK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 YLIPELCKQPYHLGWVTGTGGGISLKHGDE---IYIAPSGVQKERIQPEDMFVCDINEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 ISGPSPSKKLKKSQCTPLFMNAYTMRGAGAVIHTHSKAAVMATLLFPGREFKITHQEMIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIKKCTSGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.8%; Score 195; DB 6; Length 21 28.3%; Pred. No. 1.2e-12; tive 30; Mismatches 101; Indels
                                                                                                                                                                                                                                                                     Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 45375; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                     Malone C,
Carr GJ,
                                                  21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-GCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                              06-MAR-2002; 2002US-0362699P
21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                     Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                WPI; 2003-029926/02.
N-PSDB; ACA21321.
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Best Local Similarity
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                                                                                                                                                                                                                                                                     Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer associated nucleic acid molecules (N) and proteins (R), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and p carcinomas and cancers. AAH37196 to AAH37204 and AAB37789 represent sequences used in the exemplification of the present invention. N.B. cauchomas and cancers. AAH37196 the sequence listing were missing at time of publication, meaning no sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; prokaryotic essential gene; cell proliferation; drug design.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.2%; Score 22%; DB 4; Length 59; 100.0%; Pred. No. 4.1e-17; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 GETWEKAKTMCECYDYLFDIAVSMKKVGLDPSQLPVGENGIV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 GETWEKAKTWCECYDYLFDIAVSMKKVGLDPSQLPVGENGIV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #2978.
                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 6841; 9803pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU17451 standard; protein; 212 AA
                                                                                                                                                                                                                                                                                                                                                                                                     Birse CE,
                                                                                                                                                                                                             28-SEP-2000; 2000WO-US026524
                                                                                                                                                                                                                                                                  99US-0157137P
99US-0163280P
                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM, Barash SC,
colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus anthracis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 59 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200277183-A2.
                                                                                                    WO200122920-A2
                                                    Homo sapiens.
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03-NOV-1999;
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Query Match

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